

Appl. No. 10/028,743
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Reply to Office Action of December 29, 2003

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Amendments to the Claims:

Please withdraw claims 54 and 55, leaving claims 1-10, 12-19, 25-34, 36-43, and 49-53 pending.

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of Claims:

1. (Previously Presented) A method for analyzing expression level information, said method comprising:
 - displaying a first axis indicative of a value of a first expression level for a first expressed sequence;
 - displaying a second axis indicative of a value of a second expression level for said first expressed sequence;
 - displaying a first mark at a first position, wherein said first position has a first coordinate associated with said first axis in accordance with said first expression level of said first expressed sequence and has a second coordinate associated with said second axis in accordance with said second expression level of said first expressed sequence;
 - receiving an input of selection of said first mark; and
 - in response to said input, displaying information associated with said first expressed sequence.
2. (Previously Presented) The method of claim 1 wherein said first expressed sequence comprises a gene.
3. (Previously Presented) The method of claim 1 wherein said first expressed sequence comprises a portion of a gene.
4. (Previously Presented) The method of claim 1 further comprising displaying a second mark for a second expressed sequence.

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5. (Previously Presented) The method of claim 1 further comprising obtaining said first expression level of said first expressed sequence in a first sample and obtaining said second expression level of said first expressed sequence in a second sample.

6. (Previously Presented) The method of claim 5 wherein said obtaining said first expression level comprises:

receiving a plurality of hybridization intensities associated with at least a pair of a perfect match probe and a mismatch probe, said perfect match probe being perfectly complementary to said first expressed sequence and said mismatch probe having at least one base mismatch with said first expressed sequence, and said plurality of hybridization intensities indicating a plurality of hybridization affinities at least between said perfect match probe and said first expressed sequence and between said mismatch probe and said first expressed sequence;

associating said plurality of hybridization intensities for said perfect match probe and said mismatch probe; and

obtaining said first expression level for said first expressed sequence based on at least information associated with said plurality of hybridization intensities.

7. (Previously Presented) The method of claim 6 further comprising: associating a difference threshold and a difference between said plurality of hybridization intensities of said perfect match and said mismatch probes.

8. (Previously Presented) The method of claim 7 further comprising: associating a ratio threshold and a quotient of said plurality of hybridization intensities of said perfect match probe and said mismatch probe.

9. (Previously Presented) The method of claim 6 further comprising: for each of said at least a pair of a perfect match probe and a mismatch probe,

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counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold;

computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity;

estimating a difference of said perfect match probe intensity and said mismatch probe intensity.

10. (Previously Presented) The method of claim 9 further comprising:
for each of said at least a pair of a perfect match probe and a mismatch probe, obtaining an average of said differences for said at least a pair of a perfect match probe and a mismatch probe; and
obtaining said first expression level of said first expressed sequence based on at least information associated with said average of said differences.

11. (Canceled)

12. (Previously Presented) The method of claim 1 further comprising:
in response to said input, displaying said information associated with said first expressed sequence; said information comprising an identifier for said first expressed sequence.

13. (Previously Presented) The method of claim 12 wherein said identifier for said first expressed sequence comprises a GenBank accession number.

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14. (Previously Presented) The method of claim 12 wherein said retrieved information associated with said first expressed sequence comprises a GenBank database record for said first expressed sequence.

15. (Previously Presented) The method of claim 5 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

16. (Previously Presented) The method of claim 15 wherein said particular characteristic comprises a disease state.

17. (Original) The method of claim 15 wherein said particular characteristic comprises a treatment strategy for a disease.

18. (Previously Presented) The method of claim 15 wherein said particular characteristic is a stage of a disease.

19. (Previously Presented) The method of claim 1 further comprising:
displaying a third axis in a three-dimensional display environment wherein said first position of said first mark has a third coordinate associated with said third axis in accordance with a third expression level of said first expressed sequence.

20.-24. (Canceled)

25. (Previously Presented) A computer-readable medium including instructions for analyzing expression level information comprising:

one or more instructions for displaying a first axis indicative of a value of a first expression level for a first expressed sequence;

one or more instructions for displaying a second axis indicative of a value of a second expression level for said first expressed sequence;

one or more instructions for displaying a first mark at a first position, wherein said first position has a first coordinate associated with said first axis in accordance with said first expression level of said first expressed sequence and has a second coordinate associated

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with said second axis in accordance with said second expression level of said first expressed sequence;

one or more instructions for receiving an input of selection of said first mark; and
one or more instructions for, in response to said input, displaying information associated with said first expressed sequence.

26. (Previously Presented) The computer-readable medium of claim 25 wherein said first expressed sequence comprises a gene.

27. (Previously Presented) The computer-readable medium of claim 25 wherein said first expressed sequence comprises a portion of a gene.

28. (Previously Presented) The computer-readable medium of claim 25 further comprising one or more instructions for displaying a second mark for a second expressed sequence.

29. (Previously Presented) The computer-readable medium of claim 25 further comprising one or more instructions for obtaining said first expression level of said first expressed sequence in a first sample and obtaining said second expression level of said first expressed sequence in a second sample.

30. (Previously Presented) The computer-readable medium of claim 29 wherein said obtaining said first expression level comprises:

one or more instructions for receiving a plurality of hybridization intensities associated with at least a pair of a perfect match probe and a mismatch probe, said perfect match probe being perfectly complementary to said first expressed sequence and said mismatch probe having at least one base mismatch with said first expressed sequence, and said plurality of hybridization intensities indicating a plurality of hybridization affinities at least between said perfect match probe and said first expressed sequence and between said mismatch probe and said first expressed sequence;

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one or more instructions for associating said plurality of hybridization intensities for said perfect match probe and said mismatch probe; and

one or more instructions for obtaining said first expression level for said first expressed sequence based on at least information associated with said plurality of hybridization intensities.

31. (Previously Presented) The computer-readable medium of claim 30 further comprising:

one or more instructions for associating a difference threshold and a difference between said plurality of hybridization intensities of said perfect match and said mismatch probes.

32. (Previously Presented) The computer-readable medium of claim 31 further comprising:

one or more instructions for associating a ratio threshold and a quotient of said plurality of hybridization intensities of said perfect match probe and said mismatch probe.

33. (Previously Presented) The computer-readable medium of claim 30 further comprising:

for each of said at least a pair of a perfect match probe and a mismatch probe,
one or more instructions for counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

one or more instructions for counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold;

one or more instructions for computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity;

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one or more instructions for estimating a difference of said perfect match probe intensity and said mismatch probe intensity.

34. (Previously Presented) The computer-readable medium of claim 33 further comprising:

one or more instructions, for each of said at least a pair of a perfect match probe and a mismatch probe, for obtaining an average of said differences for said at least a pair of a perfect match probe and a mismatch probe; and

one or more instructions for obtaining said first expression level of said first expressed sequence based on at least information associated with said average of said differences.

35. (Canceled)

36. (Previously Presented) The computer-readable medium of claim 25 further comprising:

one or more instructions for, in response to said input, displaying said information associated with said first expressed sequence; said information comprising an identifier for said first expressed sequence.

37. (Previously Presented) The computer-readable medium of claim 36 wherein said identifier for said first expressed sequence comprises a GenBank accession number.

38. (Previously Presented) The computer-readable medium of claim 36 wherein said retrieved information associated with said first expressed sequence comprises a GenBank database record for said first expressed sequence.

39. (Previously Presented) The computer-readable medium of claim 29 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

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40. (Previously Presented) The computer-readable medium of claim 39 wherein said particular characteristic comprises a disease state.

41. (Previously Presented) The computer-readable medium of claim 39 wherein said particular characteristic comprises a treatment strategy for a disease.

42. (Previously Presented) The computer-readable medium of claim 39 wherein said particular characteristic is a stage of a disease.

43. (Previously Presented) The computer-readable medium of claim 25 further comprising:

one or more instructions for displaying a third axis in a three-dimensional display environment wherein said first position of said first mark has a third coordinate associate with said third axis in accordance with a third expression level of said first expressed sequence.

44.-48. (Canceled)

49. (Previously Presented) The method for analyzing expression level information, the method comprising:

displaying a first axis indicative of a value of a first expression level for a first expressed sequence;

displaying a first mark at a first position, the first position associated with a first coordinate related to the first axis in accordance with the first expression level of the first expressed sequence;

receiving an input of selection of the first mark; and
in response to the input, displaying information associated with the first expressed sequence.

50. (Previously Presented) A method for analyzing expression level information, the method comprising:

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displaying a first axis indicative of a value of a first expression level for a first expressed sequence;

displaying a second axis indicative of a value of a second expression level for the first expressed sequence;

displaying a first mark at a first position, the first position associated with a first coordinate related to the first axis in accordance with the first expression level of the first expressed sequence and associated with a second coordinate related to the second axis in accordance with the second expression level of the first expressed sequence;

receiving an input of selection of the first mark; and

in response to at least the input, retrieving information associated with the first expressed sequence.

51. (Previously Presented) The method of claim 50 wherein the retrieving information comprises sending an query to a website.

52. (Previously Presented) The method of claim 51 wherein the website is a GenBank website.

53. (Previously Presented) The method of claim 52, and further comprising displaying the retrieved information associated with the first expressed sequence.

54. (Withdrawn) A method for analyzing expression level information, the method comprising:

displaying a first axis indicative of a value of a first expression level for a first expressed sequence;

displaying a first mark at a first position, the first position associated with a first coordinate related to the first axis in accordance with the first expression level of the first expressed sequence;

generating a sound associated with the first mark, the sound indicative of a second expression level for the first expressed sequence.

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55. (Withdrawn) A method for analyzing expression level information, the method comprising:

displaying a first axis indicative of a value of a first expression level for a first expressed sequence;

displaying a first mark at a first position, the first position associated with a first coordinate related to the first axis in accordance with the first expression level of the first expressed sequence;

generating a sound associated with the first mark, the sound indicative of a second expression level for the first expressed sequence;

receiving an input of selection of the first mark; and

in response to the input, displaying information associated with the first expressed sequence.